AMENDMENT TO THE CLAIMS

Please amend the claims as follows.

Please cancel claims 5, 11, 15, 63 to 67 and 125 to 129, without prejudice or disclaimer.

This listing of claims will replace all prior versions, and listing, of claims in the application:

Claim 1 (currently amended): An isolated or recombinant nucleic acid comprising (a) a sequence having at least or about 95% **[[**90%**]]** sequence identity to ~~a sequence as set forth in~~ SEQ ID NO:1, wherein the nucleic acid encodes a polypeptide having alpha amylase activity; and (b) sequences complementary to (a).

Claim 2 (currently amended): An isolated or recombinant nucleic acid comprising (a) a sequence encoding a polypeptide having alpha amylase activity, wherein the complement of said sequence hybridizes under highly stringent conditions ~~of high stringency~~ to SEQ ID NO:1, and (b) sequences complementary to (a), wherein the highly stringent conditions ~~of high stringency~~ comprise a hybridization under conditions comprising a buffer comprising 0.1X SSC, 0.5% SDS, 0.15 NaCl, for 15 minutes at about 72°C, and a wash step ~~comprising a wash for 30 minutes at room temperature in a solution comprising 150 mM NaCl, 20 mM Tris hydrochloride, pH 7.8, 1 mM Na_2EDTA, 0.5% SDS, followed by a 30 minute wash in fresh solution;~~

~~wherein the sequence has at least or about 90% sequence identity to a sequence as set forth in SEQ ID NO:1~~.

Claims 3 to 5 (canceled)

Claim 6 (currently amended): The isolated or recombinant nucleic acid of claim 1 **[[**2**]]**, wherein said sequence has at least about 97% sequence identity to ~~a sequence as set forth in~~ SEQ ID NO:1.

Claims 7 to 11 (canceled)

Claim 12 (currently amended): The isolated or recombinant nucleic acid of claim 6 [[15]], wherein said sequence has at least about 98% sequence identity to ~~a sequence as set forth in~~ SEQ ID NO:1.

Claim 13 and 15 (canceled)

Claim 16 (previously presented): The isolated or recombinant nucleic acid of claim 1, wherein the sequence identity is determined using a sequence comparison algorithm comprising FASTA version 3.0t78 with the default parameters.

Claims 17 to 28 (canceled)

Claim 29 (currently amended): An isolated or recombinant nucleic acid encoding a polypeptide having an amino acid sequence having at least about 95% sequence identity to ~~a sequence as set forth in~~ SEQ ID NO:2, wherein the polypeptide is capable of hydrolyzing a starch to a sugar.

Claims 30 to 46 (canceled)

Claim 47 (currently amended): A method of producing a recombinant polypeptide comprising the steps of introducing a nucleic acid encoding the polypeptide into a host cell under conditions that allow expression of the polypeptide, wherein the nucleic acid comprises the sequence of claim 1 ~~or claim 2~~.

Claim 48 (currently amended): A method of producing and recovering a recombinant polypeptide comprising the steps of: introducing a nucleic acid as set forth in claim 1 ~~or claim 2~~ operably linked to a promoter, into a host cell under conditions that allow expression of the polypeptide, and recovering the recombinant polypeptide.

Claim 49 (currently amended): A method of generating a variant polynucleotide comprising: obtaining a nucleic acid as set forth in claim 1 or claim 2 and modifying one or more nucleotides in said polynucleotide to another nucleotide, deleting one or more nucleotides in said polynucleotide, or adding one or more nucleotides to said polynucleotide.

Claim 50 (currently amended): The method of claim 49, wherein the modifications are introduced by a method selected from the group consisting of: error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, Gene Site Saturation Mutagenesis (GSSM) ~~Mutagenesis™ (GSSM™)~~ and any combination of these methods.

Claim 51 (withdrawn): The method of claim 50, wherein the modifications are introduced by error-prone PCR.

Claim 52 (withdrawn): The method of claim 50, wherein the modifications are introduced by shuffling.

Claim 53 (withdrawn): The method of claim 50, wherein the modifications are introduced by oligonucleotide-directed mutagenesis.

Claim 54 (withdrawn): The method of claim 50, wherein the modifications are introduced by assembly PCR.

Claim 55 (withdrawn): The method of claim 50, wherein the modifications are introduced by sexual PCR mutagenesis.

Claim 56 (withdrawn): The method of claim 50, wherein the modifications are introduced by *in vivo* mutagenesis.

Claim 57 (withdrawn): The method of claim 50, wherein the modifications are introduced by cassette mutagenesis.

Claim 58 (withdrawn): The method of claim 50, wherein the modifications are introduced by recursive ensemble mutagenesis.

Claim 59 (withdrawn): The method of claim 50, wherein the modifications are introduced by exponential ensemble mutagenesis.

Claim 60 (withdrawn): The method of claim 50, wherein the modifications are introduced by site-specific mutagenesis.

Claim 61 (withdrawn): The method of claim 50, wherein the modifications are introduced by gene reassembly.

Claim 62 (currently amended): The method of claim 50, wherein the modifications are introduced by Gene Site Saturation Mutagenesis (GSSM) ~~Mutagenesis™ (GSSM™)~~.

Claims 63 to 67 (canceled)

Claim 68 (withdrawn): A method for comparing a first sequence to a second sequence comprising the steps of: reading the first sequence and the second sequence through use of a computer program which compares sequences; and determining differences between the first sequence and the second sequence with the computer program, wherein said first sequence comprises a sequence as set forth in claim 1 or claim 2.

Claim 69 (withdrawn): The method of claim 68, wherein the step of determining differences between the first sequence and the second sequence further comprises the step of identifying polymorphisms.

Claim 70 (withdrawn): A method for identifying a feature in a sequence comprising the steps of: reading the sequence using a computer program which identifies one or more features in a sequence; and identifying one or more features in the sequence with the computer program, wherein the sequence comprises a sequence as set forth in claim 1 or claim 2.

Claim 70 (currently amended): A method for identifying a feature in a sequence comprising the steps of: reading the sequence using a computer program which identifies one or more features in a sequence; and identifying one or more features in the sequence with the computer program, wherein the sequence comprises the [[a]] sequence of ~~as set forth in~~ claim 1 or claim 2.

Claim 71 (withdrawn): A method of hydrolyzing a starch linkage comprising contacting a substance comprising the starch with a polypeptide encoded by the nucleic acid of claim 1 or claim 2, under conditions which facilitate the hydrolysis of the starch.

Claim 72 (withdrawn): A method of catalyzing the breakdown of a starch, comprising the step of contacting a sample comprising starch with a polypeptide encoded by the nucleic acid of claim 1 or claim 2; under conditions which facilitate the breakdown of the starch.

Claim 73 (withdrawn): An assay for identifying a polypeptide having alpha amylase activity, wherein the polypeptide is encoded by a subsequence of the nucleic acid of claim 1 or claim 2, said assay comprising the steps of:

contacting the polypeptide with a substrate molecule under conditions which allow the polypeptide to function as an alpha amylase; and

(b) detecting either a decrease in an amount of a substrate or an increase in an amount of a reaction product which results from a reaction between said polypeptide and said substrate; wherein

a decrease in the amount of the substrate or an increase in the amount of the reaction product identifies a functional polypeptide.

Claim 74 (currently amended): A nucleic acid probe comprising a nucleic acid that ~~comprising a sequence (a) as set forth in claim 1 or claim 2; (b) having at least 97% sequence identity to SEQ ID NO:1 over at least 75 consecutive residues; (c) having at least 95% sequence identity to SEQ ID NO:1 over at least 150 consecutive residues; (d) having at least 90% sequence identity to SEQ ID NO:1 over at least 300 consecutive residues; or (e) sequences complementary to (a), (b) or (c),~~

~~wherein the nucleic acid probe~~ specifically hybridizes under highly stringent conditions to an amylase-encoding nucleic acid as set forth in claim 1 or claim 2, and the highly stringent conditions comprise a hybridization under conditions comprising 0.1X SSC, 0.5% SDS, 0.15 NaCl, for 15 minutes at about 72°C, and a wash step ~~comprising a wash for 30 minutes at room temperature in a solution comprising 150 mM NaCl, 20 mM Tris hydrochloride, pH 7.8, 1 mM Na_2EDTA, 0.5% SDS, followed by a 30 minute wash in fresh solution~~.

Claim 75 (previously presented): The probe of claim 74, wherein the oligonucleotide comprises DNA or RNA.

Claim 76 to 86 (canceled)

Claim 87 (previously presented): The probe of claim 74, wherein the probe further comprises a detectable isotopic label or a detectable non-isotopic label.

Claim 88 (previously presented): The probe of claim 87, wherein the probe further comprises a detectable non-isotopic label selected from the group consisting of a fluorescent molecule, a chemiluminescent molecule, an enzyme, a cofactor, an enzyme substrate, and a hapten.

Claim 89 to 94 (canceled)

Claim 95 (withdrawn): A method for modifying small molecules, comprising the step of mixing at least one polypeptide having alpha amylase activity encoded by the nucleic acid of claim 1 or claim 2; with at least one small molecule to produce at least one modified small molecule via at least one biocatalytic reaction.

Claim 96 (withdrawn): The method of claim 95, wherein the at least one polypeptide comprises a plurality of polypeptides and the at least one small molecule comprises a plurality of small molecules, whereby a plurality of modified small molecules are produced via a plurality of biocatalytic reactions to form a library of modified small molecules.

Claim 97 (withdrawn): The method of 96, further comprising the step of testing the library to determine if a particular modified small molecule, which exhibits a desired activity is present within the library.

Claim 98 (withdrawn): The method of claim 97 wherein the step of testing the library further comprises the steps of: systematically eliminating all but one of the biocatalytic reactions used to produce a portion of the plurality of the modified small molecules within the library by testing the portion of the modified small molecule for the presence or absence of the particular modified small molecule with the desired activity, and identifying a specific biocatalytic reaction which produces the particular modified small molecule of desired activity.

Claim 99 (withdrawn): The method of claim 98 wherein the specific biocatalytic reaction, which produces the modified small molecule of desired activity is repeated.

Claim 100 (withdrawn): The method of claim 93 wherein the biocatalytic reactions are conducted with a group of biocatalysts that react with distinct structural moieties found within the at least one small molecule; each biocatalyst is specific for a particular structural moiety or a group of

related structural moieties; and each biocatalyst reacts with a plurality of small molecules which contain the particular structural moiety specific to the particular biocatalyst.

Claim 101 (previously presented): A cloning vector comprising the nucleic acid of claim 1 or claim 2.

Claim 102 (currently amended): An isolated [[A]] host cell transformed or transfected with ~~comprising~~ the nucleic acid of claim 1 or claim 2.

Claim 103 (previously presented): An expression vector capable of replicating in a host cell comprising the nucleic acid of claim 1 or claim 2.

Claim 104 (currently amended): A cloning vector as claimed in claim 101 ~~or 103~~, wherein the cloning vector comprises a viral vector, a plasmid, a phage, a phagemid, a cosmids, a fosmid, a bacteriophage, an artificial chromosome, an adenovirus vector, a retroviral vector, or an adeno-associated viral vector.

Claim 105 (currently amended): An isolated [[A]] host cell transformed or transfected with ~~comprising~~ an expression vector as claimed in claim 103.

Claim 106 (currently amended): An isolated [[A]] host cell as claimed in claim 102 ~~or 105~~, wherein the host is selected from the group consisting of prokaryotes, eukaryotes, funguses, yeasts, plants and non-human metabolically rich hosts.

Claim 107 (withdrawn): A method for liquefying a starch-comprising composition comprising the step of contacting the starch with a polypeptide having alpha amylase activity encoded by the nucleic acid of claim 1 or claim 2.

Claims 108 to 110 (canceled)

Claim 111 (withdrawn): A method for washing an object comprising the step of contacting said object with a polypeptide having alpha amylase activity encoded by the nucleic acid of claim 1 or claim 2 under conditions sufficient for said washing.

Claim 112 (withdrawn): A method for textile desizing comprising the step of contacting said textile with a polypeptide having alpha amylase activity encoded by the nucleic acid of claim 1 or claim 2 under conditions sufficient for said desizing.

Claim 113 (withdrawn): A method for the treatment of lignocellulosic fibers comprising the step of contacting the fibers with a polypeptide having alpha amylase activity encoded by the nucleic acid of claim 1 or claim 2, in an amount effective for improving a fiber property.

Claim 114 (withdrawn): A method for enzymatic deinking of recycled paper pulp, comprising the step of contacting the recycled paper pulp with a polypeptide having alpha amylase activity encoded by the nucleic acid of claim 1 or claim 2 in an amount which is efficient for effective deinking of the recycled paper pulp.

Claim 115 (currently amended): A method for starch liquefaction comprising contacting said starch with **[[with]]** a polypeptide having alpha amylase activity encoded by the nucleic acid of claim 1 or claim 2 under conditions sufficient for said liquefaction.

Claim 116 (canceled)

Claim 117 (currently amended): The method of claim 107, wherein the polypeptide having alpha amylase activity encoded by the nucleic acid has the **[[a]]** sequence of ~~as set forth in~~ SEQ ID NO: 2.

Claim 118 (withdrawn): A method for producing a high-maltose or a high-glucose syrup or a mixed syrup comprising: liquefying starch using an effective amount of a polypeptide having alpha amylase activity encoded by the nucleic acid of claim 1 or claim 2 to obtain a soluble starch hydrolysate; and saccharifying the soluble starch hydrolysate, thereby resulting in a syrup.

Claim 119 (withdrawn): The method of claim 107, wherein the starch is from a material comprising rice, germinated rice, corn, barley, wheat, legumes or sweet potato.

Claim 120 (withdrawn): The method of claim 107, further comprising addition of a second alpha amylase or a beta amylase or a combination thereof.

Claim 121 (withdrawn): A method of increasing the flow of production fluids from a subterranean formation by removing a viscous, starch-containing, damaging fluid formed during production operations and found within the subterranean formation which surrounds a completed well bore comprising:

allowing production fluids to flow from the well bore;

reducing the flow of production fluids from the formation below expected flow rates;

formulating an enzyme treatment by blending together an aqueous fluid and a polypeptide having alpha amylase activity encoded by the nucleic acid of claim 1 or claim 2;

pumping the enzyme treatment to a desired location within the well bore and allowing the enzyme treatment to degrade the viscous, starch-containing, damaging fluid, such that the enzyme-treated production fluid can be removed from the subterranean formation to the well surface.

Claim 122 (currently amended): The method of claim 121, wherein the enzyme has the **[[a]]** sequence of ~~as set forth in~~ SEQ ID NO:2.

Claims 123 to 129 (canceled)

Claim 130 (currently amended): A method of producing a recombinant polypeptide comprising the steps of

(a) introducing a nucleic acid encoding the polypeptide into a host cell under conditions that allow expression of the polypeptide, wherein the nucleic acid comprises the sequence of claim 2 ~~128 or claim 129~~, or,

(b) introducing [[a]] the nucleic acid ~~as set forth in claim 128 or claim 129~~ operably linked to a promoter [[,]] into a host cell under conditions that allow expression of the polypeptide, thereby producing a recombinant ~~and recovering the~~ polypeptide.

Claim 131 (currently amended): An expression vector comprising the nucleic acid of claim 1 or claim 2 ~~128 or claim 129~~, wherein the ~~optionally the vector is an~~ expression vector ~~or a cloning vector, or optionally the vector~~ comprises a viral vector, a plasmid, a phage, a phagemid, a cosmids, a fosmid, a bacteriophage, an artificial chromosome, an adenovirus vector, a retroviral vector, or an adeno-associated viral vector.

Claim 132 (currently amended): A host cell comprising the nucleic acid of claim 1 or claim 2 ~~128 or claim 129~~, wherein ~~optionally~~ the cell is a prokaryote cell, a eukaryote cell, a fungus cell, a yeast cell, a plant cell or a non-human metabolically rich host cell.